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OM nucleic - nucleic search, using SW model

Run on: March 19, 2005, 20:14:54 ; Search time 195.768 Seconds
(without alignments)
8299.718 Million cell updates/sec

Title: US-09-826-791A-1

Perfect score: 993
Sequence: 1 atggaaccacaaatgacacccct.....gaaggaacaagaatataa 993

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818139359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/prodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/prodata/1/ina/5B_COMB.seq: *
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6: /cgn2_6/prodata/1/ina/5B_COMB.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	989.8	99.7	1401	4 US-09-585-876-1	Sequence 1, Appl
2	145.2	14.6	1578	3 US-09-044-404A-1	Sequence 1, Appl
3	145.2	14.6	1578	4 US-09-586-924-1	Sequence 1, Appl
4	99.4	10.0	1020	4 US-09-170-496D-31	Sequence 31, Appl
5	99.4	10.0	1900	4 US-09-016-434-1484	Sequence 1484, Ap
6	99.4	10.0	1901	4 US-08-153-848-43	Sequence 43, Ap
7	99.4	10.0	1901	3 US-09-299-843A-43	Sequence 43, Appl
8	99.4	10.0	1901	3 US-09-088-337B-43	Sequence 43, Appl
9	99.4	10.0	1901	5 PCT-US93-11153-43	Sequence 43, Appl
10	99.4	10.0	2453	5 PCT-US95-07180-1	Sequence 1, Appl
11	96.2	9.7	1020	4 US-09-170-496D-181	Sequence 181, App
12	92.3	9.3	1255	1 US-08-097-938-3	Sequence 3, Appl
13	92.3	9.3	1255	1 US-08-476-000-3	Sequence 3, Appl
14	92.3	9.3	1255	1 US-08-472-840-3	Sequence 3, Appl
15	92.3	9.3	1255	2 US-08-476-976-3	Sequence 3, Appl
16	92.3	9.3	1255	3 US-08-474-410-3	Sequence 3, Appl
17	92.3	9.3	1255	3 US-08-486-673B-3	Sequence 3, Appl
18	90.9	9.1	1224	2 US-08-742-404A-1	Sequence 1, Appl
19	90.9	9.1	1414	1 US-08-476-000-62	Sequence 62, Appl
20	90.9	9.1	1414	1 US-08-472-840-62	Sequence 62, Appl
21	90.9	9.1	1414	2 US-08-476-976-62	Sequence 62, Appl
22	90.9	9.1	1414	3 US-08-474-410-62	Sequence 62, Appl
23	90.9	9.1	1414	3 US-08-486-673B-62	Sequence 62, Appl
24	85.6	8.6	1567	3 US-08-889-108-16	Sequence 16, Appl
25	85.6	8.6	1567	5 PCT-US94-10358-16	Sequence 16, Appl
26	85.6	8.6	2706	2 US-08-454-549-1	Sequence 1, Appl
27	85.6	8.6	2706	3 US-08-454-552-1	Sequence 1, Appl

28	85.2	8.6	1452	1 US-08-149-093A-3	Sequence 3, Appl
29	85.2	8.6	1452	1 US-08-911-245-3	Sequence 3, Appl
30	85.2	8.6	1452	1 US-08-553-058C-3	Sequence 3, Appl
31	85.2	8.6	1452	2 US-08-514-451A-3	Sequence 3, Appl
32	85.2	8.6	1452	3 US-09-170-331-3	Sequence 3, Appl
33	85.2	8.6	1452	3 US-09-510-473-3	Sequence 3, Appl
34	85.2	8.6	1452	3 US-09-048-916B-3	Sequence 3, Appl
35	84.4	8.5	1551	4 US-09-016-434-1239	Sequence 1239, Ap
36	84.4	8.5	1551	4 US-09-023-655-1186	Sequence 1186, Ap
37	84.4	8.5	1780	4 US-09-054-272-1	Sequence 1, Appl
38	83.2	8.4	1098	4 US-09-170-496D-225	Sequence 225, App
39	82.4	8.3	2706	4 US-08-676-351-1	Sequence 1, Appl
40	81.6	8.2	1098	4 US-09-170-496D-117	Sequence 117, App
41	81.6	8.2	1597	2 US-08-724-974A-1	Sequence 1, Appl
42	81.6	8.2	1697	4 US-09-364-425B-26	Sequence 26, Appl
43	81.4	8.2	1164	4 US-09-170-496B-107	Sequence 107, App
44	81.4	8.2	1164	4 US-09-170-496D-221	Sequence 221, App
45	81.4	8.2	2051	4 US-09-016-434-1259	Sequence 1259, Ap

ALIGNMENTS

RESULT 1					
US-09-585-876-1					
Sequence 1, Application US/09585876					
Patent No. 6586205					
GENERAL INFORMATION:					
APPLICANT: Gluckemann, Maria Alexandra					
APPLICANT: Siles-Santillago, Immaculada					
TITLE OF INVENTION: 43239, A No. 6586205el GPCR-Like Molecule and					
TITLE OF INVENTION: Uses thereof					
FILE REFERENCE: 5800-88					
CURRENT APPLICATION NUMBER: US/09/585, 876					
CURRENT FILING DATE: 2000-06-01					
EARLIER APPLICATION NUMBER: 60/182, 061					
EARLIER FILING DATE: 2000-02-11					
NUMBER OF SEQ ID NOS: 2					
SOFTWARE: FASTSEQ for Windows Version 3.0					
SEQ ID NO 1					
LENGTH: 1401					
TYPE: DNA					
ORGANISM: Homo sapiens					
FEATURE:					
NAME/KEY: CDS					
LOCATION: (197) ... (1237)					
US-09-585-876-1					
Query Match					
Best Local Similarity: 99.7%; Score 989.8; DB 4; Length 1401;					
Best Local Similarity: 99.8%; Pred. No. 8.2e-307;					
Matches 991; Conservative 0; Mismatches 2; Indels 0; Gaps 0;					
QY	1	ATGGAACCAATGGACCTTCAGCATTAAACAAGAGAGAACTGCAATTTGAAACTTC	60		
DB	245	ATGGAACCAATGGACCTTCAGCATTAAACAAGAGAGAACTGCAATTTGAAACTTC	304		
QY	61	AAGAGAAATTTTCCCAATGATATATATATATATATATTTTGGGGAGCTTGGAAAT	120		
DB	305	AAGAGAAATTTTCCCAATGATATATATATATATATATTTTGGGGAGCTTGGAAAT	364		
QY	121	GGGTTTCATATATATTTTCCGAGCCTTATTAAGAAGTCCCATCTGGAACGTTTC	180		
DB	365	GGGTTTCATATATATTTTCCGAGCCTTATTAAGAAGTCCCATCTGGAACGTTTC	424		
QY	181	ATGCTAATCTGGCATTTCAGATCTCGTTTCATTAAGACGCTTCCTTCAGGGCTGAC	240		
DB	425	ATGCTAATCTGGCATTTCAGATCTCGTTTCATTAAGACGCTTCCTTCAGGGCTGAC	484		
QY	241	TATATCTTAAAGGCTCCAAATTTGAGATTTGAGAGCTGGCTGAGATTTATCTTAT	300		
DB	485	TATATCTTAAAGGCTCCAAATTTGAGATTTGAGAGCTGGCTGAGATTTATCTTAT	544		
QY	301	TCTTTATATGTCACATGATGACAGATATTTATTTCTGACCGTGGCTGAGTGTGCGCT	360		

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Db      545 TCCTGTATGTCAACATGTAAGAGATATTATTTCCGACCGGTGAGGTGTGCGT 604
Qy      361 TTCTGGCAATGGTTCACCCCTTTCGGCTTCTGATGTCAACAGATCAAGAGTCTGG 420
Db      605 TTCTGGCAATGGTTCACCCCTTTCGGCTTCTGATGTCAACAGATCAAGAGTCTGG 664
Qy      421 ATCCTGTGGATCATATGATGATCCTTATATAGTGGTCCCAATATATGCTCTGAGAGT 480
Db      665 ATCCTGTGGATCATATGATGATCCTTATATAGTGGTCCCAATATATGCTCTGAGAGT 724
Qy      481 GGCTGTAGAGAAACGGCACTGTCACTATGCTTAGAGTGAATCTCTATATAATGCT 540
Db      725 GGCTGTAGAGAAACGGCACTGTCACTATGCTTAGAGTGAATCTCTATATAATGCT 784
Qy      541 AGCTGACAGACATGAATCTATATGCTGTGTGTGGCTGCTGCTGCTGCTGCTGCTGCT 600
Db      785 AGCTGACAGACATGAATCTATATGCTGTGTGTGGCTGCTGCTGCTGCTGCTGCTGCT 844
Qy      601 CTCAGCATCTGTATCTGTGATCATTCGGGTTCTGTTAAAGTGAAGTCCAGAAATCG 660
Db      845 CTCAGCATCTGTATCTGTGATCATTCGGGTTCTGTTAAAGTGAAGTCCAGAAATCG 904
Qy      661 GGGCTGCGGGTTCCTCAACAGAAAGCACTGACACATCATCATCACTTATCATCTTC 720
Db      905 GGGCTGCGGGTTCCTCAACAGAAAGCACTGACACATCATCATCACTTATCATCTTC 964
Qy      721 TTCTGTGTTTCTGCTGCTTCACTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db      965 TTCTGTGTTTCTGCTGCTTCACTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1024
Qy      781 GGTTTATGACAAAGACAGTCAATTAAGCTTGTGTTTCACTGCTGCTGCTGCTGCTGCT 840
Db      1025 GGTTTATGACAAAGACAGTCAATTAAGCTTGTGTTTCACTGCTGCTGCTGCTGCTGCT 1084
Qy      841 AATGCTGCTTCACTCTGCTCTATTAATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Db      1085 AATGCTGCTTCACTCTGCTCTATTAATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1144
Qy      901 AATGCTGCTTCACTGCTGCTCTATTAATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db      1145 AATGCTGCTTCACTGCTGCTCTATTAATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1204
Qy      961 AGTGTGTGTTGAAGAAAGAAAGAGTATA 993
Db      1205 AGTGTGTGTTGAAGAAAGAAAGAGTATA 1237

RESULT 2
US-09-044-404A-1
/ Sequence 1, Application US/09044404A
/ Patent No. 6200775
/ GENERAL INFORMATION:
/ APPLICANT: SATHE, GANESH
/ APPLICANT: HALSEY, WENDY
/ APPLICANT: ELLIS, CATHERINE
/ APPLICANT: AMES, ROBERT
/ APPLICANT: FOLEY, JAMES
/ APPLICANT: SARAU, HENRY
/ TITLE OF INVENTION: CDNA CLONE HMTF81 THAT ENCODES
/ TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
/ NUMBER OF SEQUENCES: 2
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSES: SmithKline Beecham Corporation
/ STREET: 790 Swedeland Road, P.O. Box 1539
/ CITY: King of Prussia
/ STATE: PA
/ COUNTRY: USA
/ ZIP: 19406
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS

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/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/044,404A
/ FILING DATE: MARCH 19, 1998
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/844,795
/ FILING DATE: APRIL 22, 1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Han, William T.
/ REGISTRATION NUMBER: 34,344
/ REFERENCE/DOCKET NUMBER: GH-70001-1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 610-270-5219
/ TELEFAX: 610-270-5090
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1578 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ US-09-044-404A-1

Query Match      14.6%; Score 145.2; DB 3; Length 1578;
Best Local Similarity 51.5%; Pred. No. 1,1e-35;
Matches 451; Conservative 0; Mismatches 398; Indels 27; Gaps 4;

Qy      45 CACATTTGAAACCTTCAGAGAGAAATTTCCCAATGTATATCTGATTAATTTTCTG 104
Db      514 CACATTTGATGATCTTCGCAATCAAGTATATCACTTGTATCTATGATCTGTGTGT 573
Qy      105 GGGAGTCTGGGAAATGGGTTGTCATATATGTTTCTGACGCTTATAGAGTGCAC 164
Db      574 AGGCTCTTGGGAAATGGGTTGTCATATGTCCTATATAAACCTATACAGAAATGC 633
Qy      165 ATCTGGAAGTTTCAATGCTAATCTGCAATTCGCAATTCCTGCTTCAATAGCAGCT 224
Db      634 AGCTTCGAAGTATACATGATTAATTTAGCAGTACAGATCTATTTGTGTGCAACT 693
Qy      225 TCCCTCAGGGCTGACTATATATCTTAGAGGCTCCCAATGTGATATTTGAGACCTG 284
Db      694 GCCTTCGGTGTGTATATATGTCACAAAGGATTTGGCTCTTGTGTGCTTGTG 753
Qy      285 CAGATATATCTTATCTTGTATGTCACATGTACAGCATATTTATTTCTGACCT 344
Db      754 CCGCTCAGCAGCTATGCTTGTATGTCACACTCTATTTGAGCATCTTCTTATGAGAC 813
Qy      345 GCTGAGTGTGTGCTTCTGCAATGTTCAACCCCTTCGGCTTCTGATGACAG 404
Db      814 CATGAGCTTTTCCGGTCAATGCAATTTTTCAGTCAAGAACTTATTTGCTTAC 873
Qy      405 CATCAGAGTCTGTGATCTCTGTGGGATCATATGATCTT---ATCATGGCTTCTC 461
Db      874 ACAGAAAAGCCAGGTTGTGTGTAGGATTTGGATTTTGTGATTTGACCACTTC 933
Qy      462 AATATGCTCTGTGACATGCTGTGACGAAACGGAGTGTACATCATGCTTAGGCT 521
Db      934 TCCATTTCTATGTGCCCAACACAAAAGATGGAAAAAATATACCAAGGCTTTGAGCC 993
Qy      522 GAATCTTATTAATAATGCTAAGCTGCA-----GACATGAACATATTTGCTGTGTGT 575
Db      994 CCACAGACATATCAAACTTAAAAATCTGTTTGTGTTTCAATATATGTCATTTGTGT 1053
Qy      576 GGGCTGCTGTGCAATTTTTCACATCAGATCTGTATCTGTGATCATTCGGGTTCT 635
Db      1054 TGGCTTATCATCCTTTTGTATTAATTTGTATTAATGCTGTATCAATGATCATTTGACCTT 1113
Qy      636 GTTAAAGTGAAGTCCAGATCGGGGCTGCGGTTTCTCAACAGAGGACCTGACAC 695
Db      1114 ACTAAAAAATCATGAAAAAATATGTGTCAAG-----TCATTAAGGCTATAGGAAT 1167

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